

M.RAO

Re-RUN



1600

RAW SEQUENCE LISTING

DATE: 03/12/2003

PATENT APPLICATION: US/09/576,778B

TIME: 10:42:33

Input Set : N:\vernette\US09576778B.raw

Output Set: N:\CRF4\03122003\I576778B.raw

1 <110> APPLICANT: Schulein, Martin
 2 <111> Ejj-Invad, Mads
 3 <120> TITLE OF INVENTION: Family 9 Endo-Beta-1, 4-Glucanases
 4 <130> FILE REFERENCE: 1843.200-US
 C--> 5 <140> CURRENT APPLICATION NUMBER: US/09/576,778B
 C--> 6 <141> CURRENT FILING DATE: 2000-05-24
 7 <160> NUMBER OF SEQ ID NOS: 10
 8 <170> SOFTWARE: PatentIn version 3.1
 9 <210> SEQ ID NO: 1
 10 <211> LENGTH: 1941
 11 <212> TYPE: DNA
 12 <213> ORGANISM: Bacillus licheniformis
 13 <214> FEATURE:
 14 <215> NAME/KEY: CDS
 15 <216> LOCATION: (1)..(1938)
 16 <217> OTHER INFORMATION:
 17 <220> FEATURE:
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 19 <222> LOCATION: (1)..(27)
 20 <223> OTHER INFORMATION:
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 22 <222> LOCATION: (48)..
 23 <223> OTHER INFORMATION:
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30	Met Lys Ala Leu Cys Leu Ala Leu Leu Val Ile Phe Ser Met Ser Ile	
33	-05 -20 -15	
36	gag tgg ttt tca gaa aag acc cgt gca gct tct gct gaa gaa tat cct	96
39	Ala Ser Phe Ser Glu Lys Thr Arg Ala Ala Ser Ala Glu Glu Tyr Pro	
42	-10 -5 -1 1	
45	gat aat tat gct gaa ctg ctg caa aag tct ttg tta ttt tat gaa gca	144
48	His Asn Tyr Ala Glu Leu Leu Gln Lys Ser Leu Leu Phe Tyr Glu Ala	
51	5 10 15	
54	gag cgc tgg gga aga ctt ccg gaa aac agc cgg ctg aat tgg aga gga	192
57	Gln Arg Ser Gly Arg Leu Pro Glu Asn Ser Arg Leu Asn Trp Arg Gly	
60	20 25 30 35	
63	gac tcc ggg ctt gag gac gga aaa gac gtt ggc ctc gat tta acg gga	240
66	Asp Ser Gly Leu Glu Asp Gly Lys Asp Val Gly Leu Asp Leu Thr Gly	
69	40 45 50	
72	ggg tgg tat gat gcc ggc gac cac gtg aag ttc ggt ctg ccg atg gct	288
75	Gly Trp Tyr Asp Ala Gly Asp His Val Lys Phe Gly Leu Pro Met Ala	
78	55 60 65	

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PATENT APPLICATION: US/09/576,778B

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Input Set : N:\vernette\US09576778B.raw

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45	tat tct gcc gca atc ctg tca tgg tgg gtc tat gag tac cga gat gcc	336
46	Tyr Ser Ala Ala Ile Leu Ser Trp Ser Val Tyr Glu Tyr Arg Asp Ala	
47	75 75 80	
48	tac aaa gaa tgg ggt cag ctt gat ggg ggg cgg gac aat att aat tgg	384
49	Tyr Lys Glu Ser Gly Gln Leu Asp Ala Ala Leu Asp Asn Ile Lys Trp	
50	85 90 95	
51	gat aca gac tac ttt ctt aaa gcc cat aag gct cct tat gaa tta tgg	432
52	Ala Thr Asp Tyr Phe Leu Lys Ala His Thr Ala Pro Tyr Glu Leu Trp	
53	100 105 110 115	
54	gat cta gtc gga aat gcc gct cta gac caa gca tgg tgg ggg cca gcc	480
55	Gly Gln Val Gly Asn Gly Ala Leu Asp His Ala Trp Trp Gly Pro Ala	
56	120 125 130	
57	gat gta atg cgg atg aag cgc cct gcc tat aag atc gat gcc ggc tgt	528
58	Val Val Met Pro Met Lys Arg Pro Ala Tyr Lys Ile Asp Ala Gly Cys	
59	135 140 145	
60	caa ggg tca gac ctt gct ggt gat aca gcc gca gcc cta gca tca gca	576
61	Pro Gly Ser Asp Leu Ala Gly Gly Thr Ala Ala Ala Leu Ala Ser Ala	
62	150 155 160	
63	tca aat att ttc aag cgg aca gat tct tct tac tct gaa aaa tta cgg	624
64	Ser Ile Ile Phe Lys Pro Thr Asp Ser Ser Tyr Ser Glu Lys Leu Leu	
65	165 170 175	
66	gat cat gcc aag caa ttg tat gat ttt gcc gac cgc tac cgc ggt aaa	672
67	Ala His Ala Lys Gln Leu Tyr Asp Phe Ala Asp Arg Tyr Arg Gly Lys	
68	180 185 190 195	
69	tat tca gac tgc att aca gcc gca cag caa tat tat aat tgg tgg agc	720
70	Tyr Ser Asp Cys Ile Thr Asp Ala Gln Gln Tyr Tyr Asn Ser Trp Ser	
71	200 205 210	
72	gaa tat aaa gat gaa ctg aca tgg gga gct gtc tgg ctc tac tta gca	768
73	Gly Tyr Lys Asp Glu Leu Thr Trp Gly Ala Val Trp Leu Tyr Leu Ala	
74	215 220 225	
75	aaa gaa gaa caa caa tat ttg gat aaa gcc ctt gct tgg gtc tta gat	816
76	Thr Glu Glu Gln Gln Tyr Leu Asp Lys Ala Leu Ala Ser Val Ser Asp	
77	230 235 240	
78	tta ggc gat ccc gcc aac tgg cct tac cgc tgg aag ctc tcc tga gat	864
79	Trp Gly Asp Pro Ala Asn Trp Pro Tyr Arg Trp Thr Leu Ser Trp Asp	
80	245 250 255	
81	gat gtc aat tac gga gca cag ctg ctg ctc gct cgt cgt cga aat gat	912
82	Arg Val Thr Tyr Gly Ala Gln Leu Leu Leu Ala Arg Leu Thr Asn Asp	
83	260 265 270 275	
84	tca cgt ttt gtc aaa tct gtc gaa cgc aat ctt gat tat tgg tca aca	960
85	Ser Arg Phe Val Lys Ser Val Glu Arg Asn Leu Asp Tyr Trp Ser Thr	
86	280 285 290	
87	ggt tac agt cat aat gga agc ata gaa cgg atc aag tat aag cca gcc	1008
88	Gly Tyr Ser His Asn Gly Ser Ile Glu Arg Ile Thr Tyr Thr Pro Gly	
89	295 300 305	
90	ggg ttg gcc tgg ctt gag cag tgg gga tca ttg cga tac gct tgg aat	1056
91	Gly Leu Ala Trp Leu Glu Gln Trp Gly Ser Leu Arg Tyr Ala Ser Asn	
92	310 315 320	
93	gcc gct ttt ctc gct ttc gtt tat tcc gat tgg gtg gat aca gaa aaa	1104

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Input Set : N:\vernette\US09576778B.raw

Output Set: N:\CRF4\03122003\I576778B.raw

94	Ala Ala Phe Leu Ala Phe Val Tyr Ser Asp Trp Val Asp Thr Glu Lys	
95	325	335
96	ggc aia aga tat cgg gat ttt gct gtt cgg caa acg gac tat atg cta	1152
97	Ala Lys Arg Tyr Arg Asp Phe Ala Val Arg Gln Thr Gln Tyr Met Leu	
98	340	345
99	gga gat aat cgg cag cag cga agc ttt gtc gtt gga tac ggt aaa aat	1200
100	Gly Asp Asn Pro Gln Gln Arg Ser Phe Val Val Gly Tyr Gly Lys Asn	
101		360
102	cgg cgg aaa cat cgg cat cgc cgt aca gaa cgc ggt tca tgg gcc aat	1248
103	Pro Pro Lys His Pro His His Arg Thr Ala His Gly Ser Trp Ala Asn	
104		375
105	cag atc aat ctg cct gaa aac cat cgc cat acc cta tgc ggc gaa ata	1296
106	Gln Met Asn Val Pro Gln Asn His Arg His Thr Leu Tyr Gly Ala Leu	
107		390
108	gtc ggc ggt cgg gga agc gac cat tgg tac cga gat gac ata aca gat	1344
109	Val Gly Gly Pro Gly Arg Asp Asp Ser Tyr Arg Asp Asp Ile Thr Asp	
110		405
111	tat ggc tca aac gaa gtt cgg atc gat tat aat ggc gct ttt aac ggc	1392
112	Tyr Ala Ser Asn Gln Val Ala Ile Asp Tyr Asn Ala Ala Phe Thr Gly	
113		420
114	aac tta ggc aaa atg ttt cag ctg ttc ggc aaa ggc cat gtt cgg ctg	1440
115	Asn Val Ala Lys Met Phe Gln Leu Phe Gly Lys Gly His Val Pro Leu	
116		440
117	cct gat ttt cgg gag aag gaa aca cct gag gac gaa tat ttt gaa gag	1488
118	Pro Asp Phe Pro Gln Lys Gln Thr Pro Gln Asp Gln Tyr Phe Ala Gln	
119		455
120	gca tca atc aac aga tcc gga aac agc tat aat gaa atc cgg gag cag	1536
121	Ala Ser Ile Asn Ser Ser Gly Asn Ser Tyr Thr Gln Ile Arg Ala Gln	
122		470
123	ctc aat aac cgt tgc gga tgg cgg gaa aag aaa aac gat caa tgg tct	1584
124	Leu Asn Asn Arg Ser Gly Trp Pro Ala Lys Lys Thr Asp Gln Leu Ser	
125		485
126	ctc cgg tac tcc gtt gac ttg acc gaa gct gta gaa gag gga tat tcc	1632
127	Phe Arg Tyr Tyr Val Asp Leu Thr Gln Ala Val Gln Ala Gly Tyr Ser	
128		500
129	gcc gaa gat ata aaa gtc aca gcc ggc tat aac gaa gag gct tgg gta	1680
130	Ala Gln Asp Ile Lys Val Thr Ala Gly Tyr Asn Gln Gly Ala Ser Val	
131		520
132	tca gag ctg aag cgg cat gac gct tca aag cgc att tgc tat aca gaa	1728
133	Ser Gln Leu Lys Pro His Asp Ala Ser Lys His Ile Tyr Tyr Thr Gln	
134		535
135	gtc agc ttc acc ggg gtt ttg att tat tca ggc ggt caa tcc gcc cat	1776
136	Val Ser Phe Ser Gly Val Leu Ile Tyr Pro Gly Gly Gln Ser Ala His	
137		550
138	aaa aaa gaa gtg cag ttc cgc att tgc gca cca gac gga acc tct ttt	1824
139	Lys Lys Gln Val Gln Phe Arg Leu Ser Ala Pro Asp Gly Thr Ser Phe	
140		565
141	tgg aac cgg gaa aat gac cac tct tat cag ggt ctg tca cat gcg ctt	1872
142	Trp Asn Pro Gln Asn Asp His Ser Tyr Gln Gly Leu Ser His Ala Leu	

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142      585      590      595
144      ctc aag acg cgg tat att cct gtt tat gat gat gga cgg ctc gtt ttc      1920
146      Leu Lys Thr Arg Tyr Ile Pro Val Tyr Asp Asp Gly Arg Leu Val Phe
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149      gga cat gag ccc ggt tac tag      1941
151      Gly His Glu Pro Gly Tyr
153      615
154 <210> SEQ ID NO: 2
155 <211> LENGTH: 646
156 <212> TYPE: PRP
157 <213> ORGANISM: Bacillus licheniformis
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162      Ala Ser Phe Ser Glu Lys Thr Arg Ala Ala Ser Ala Glu Glu Tyr Pro
164      -10      -5
165      His Asn Tyr Ala Glu Leu Leu Gln Lys Ser Leu Leu Phe Tyr Glu Ala
167      5      10      15
168      Glu Arg Ser Gly Arg Leu Pro Glu Asn Ser Arg Leu Asn Trp Arg Gly
170      20      25      30      35
171      Asp Ser Gly Leu Glu Asp Gly Lys Asp Val Gly Leu Asp Leu Thr Gly
173      40      45      50
174      Gly Trp Tyr Asp Ala Gly Asp His Val Lys Phe Gly Leu Pro Met Ala
176      55      60      65
177      Tyr Ser Ala Ala Ile Leu Ser Trp Ser Val Tyr Glu Tyr Arg Asp Ala
179      70      75      80
180      Tyr Lys Glu Ser Gly Gln Leu Asp Ala Ala Leu Asp Asn Ile Lys Trp
182      85      90      95
183      Ala Thr Asp Tyr Phe Leu Lys Ala His Thr Ala Pro Tyr Glu Leu Trp
185      100      105      110      115
186      Gly Gln Val Gly Asn Gly Ala Leu Asp His Ala Trp Trp Gly Pro Ala
188      120      125      130
189      Glu Val Met Pro Met Lys Arg Pro Ala Tyr Lys Ile Asp Ala Gly Cys
191      135      140      145
192      Pro Gly Ser Asp Leu Ala Gly Gly Thr Ala Ala Ala Leu Ala Ser Ala
194      150      155      160
195      Ser Ile Ile Phe Lys Pro Thr Asp Ser Ser Tyr Ser Glu Lys Leu Leu
197      165      170      175
198      Ala His Ala Lys Gln Leu Tyr Asp Phe Ala Asp Arg Tyr Arg Gly Lys
200      180      185      190      195
201      Tyr Ser Asp Cys Ile Thr Asp Ala Gln Gln Tyr Tyr Asn Ser Trp Ser
203      200      205      210
204      Gly Tyr Lys Asp Glu Leu Thr Trp Gly Ala Val Trp Leu Tyr Leu Ala
206      215      220      225
207      Thr Glu Glu Gln Gln Tyr Leu Asp Lys Ala Leu Ala Ser Val Ser Asp
209      230      235      240
210      Trp Gly Asp Pro Ala Asn Trp Pro Tyr Arg Trp Thr Leu Ser Trp Asp
212      245      250      255
213      Asp Val Thr Tyr Gly Ala Gln Leu Leu Leu Ala Arg Leu Thr Asn Asp

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Output Set: N:\CRF4\03122003\I576778B.raw

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193      265      265      270      275
194 Ser Arg Phe Val Lys Ser Val Glu Arg Asn Leu Asp Tyr Trp Ser Thr
195      290      295      300
196 Gly Tyr Ser His Arg Gly Ser Ile Glu Arg Ile Thr Tyr Thr Pro Gly
197      295      300      305
198 Gly Leu Ala Trp Leu Glu Gln Trp Gly Ser Leu Arg Tyr Ala Ser Asn
199      310      315      320
200 Ala Ala Phe Leu Ala Phe Val Tyr Ser Asp Trp Val Asp Thr Glu Lys
201      325      330      335
202 Ala Lys Arg Tyr Arg Asp Phe Ala Val Arg Gln Thr Glu Tyr Met Leu
203      340      345      350
204 Gly Asp Asn Pro Gln Gln Arg Ser Phe Val Val Gly Tyr Gly Lys Asn
205      355      360
206 Pro Pro Lys His Pro His His Arg Thr Ala His Gly Ser Trp Ala Asn
207      365      370      375
208 Gln Met Asn Val Pro Glu Asn His Arg His Thr Leu Tyr Gly Ala Leu
209      380      385      390
210 Val Gly Gly Pro Gly Arg Asp Asp Ser Tyr Arg Asp Asp Ile Thr Asp
211      395      400      405
212 Tyr Ala Ser Asn Gln Val Ala Ile Asp Tyr Asn Ala Ala Phe Thr Gly
213      410      415      420
214 Asn Val Ala Lys Met Phe Gln Leu Phe Gly Lys Gly His Val Pro Leu
215      425      430      435
216 Pro Asp Phe Pro Gln Lys Glu Thr Pro Glu Asp Glu Tyr Phe Ala Glu
217      440      445      450
218 Ala Ser Ile Asn Ser Ser Gly Asn Ser Tyr Thr Glu Ile Arg Ala Gln
219      455      460      465
220 Leu Asn Asn Arg Ser Gly Trp Pro Ala Lys Lys Thr Asp Gln Leu Ser
221      470      475      480
222 Phe Arg Tyr Tyr Val Asp Leu Thr Gln Ala Val Glu Ala Gly Tyr Ser
223      485      490      495
224 Ala Glu Asp Ile Lys Val Thr Ala Gly Tyr Asn Gln Gly Ala Ser Val
225      500      505      510
226 Ser Gln Leu Lys Pro His Asp Ala Ser Lys His Ile Tyr Tyr Thr Glu
227      515      520      525
228 Val Ser Phe Ser Gly Val Leu Ile Tyr Pro Gly Gly Gln Ser Ala His
229      530      535      540
230 Lys Lys Glu Val Gln Phe Arg Leu Ser Ala Pro Asp Gly Thr Ser Phe
231      545      550      555
232 Trp Asn Pro Gln Asn Asp His Ser Tyr Gln Gly Leu Ser His Ala Leu
233      560      565      570
234 Leu Lys Thr Arg Tyr Ile Pro Val Tyr Arg Asp Gly Arg Leu Val Phe
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236 Gly His Glu Pro Gly Tyr
237      590      595      600
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239 <211> LENGTH: 42
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence

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VERIFICATION SUMMARY

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Input Set : N:\vernette\US09576778B.raw

Output Set: N:\CRF4\03122003\I576778B.raw

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L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0